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OM protein - protein search, using sw model

Run on: December 29, 2004, 16:12:59 ; Search time 151 Seconds
(without alignments)
21.381 Million cell updates/sec

Title: US-10-006-177-4

Perfect score: 49

Sequence: 1 FLYDNDQNV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A.GeneSeq.23Sep04:*

1: Genesegp1980s:*\n2: Genesegp1990s:*\n3: Genesegp2000s:*\n4: Genesegp2001s:*\n5: Genesegp2002s:*\n6: Genesegp2003as:*\n7: Genesegp2003bs:*\n8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	5	ABG32304 HLA-A2 as
2	49	100.0	546	4	ABG22395 Novel hum
3	49	100.0	1139	4	ABG22397 Novel hum
4	49	100.0	1526	7	AD661230 Rat Prote
5	49	100.0	1526	7	ADD44993 Rat Prote
6	49	100.0	1530	7	ADN95295 Human BEC
7	49	100.0	1531	5	ABP67994 Human col
8	49	100.0	1531	5	AAO18890 Human ova
9	49	100.0	1531	5	ABG80433 Antl-huma
10	49	100.0	1531	6	ABU56492 Lung canc
11	49	100.0	1531	6	ABR92156 Human cer
12	49	100.0	1531	7	ADD44995 Human Pro
13	49	100.0	1531	7	AD661232 Human Pro
14	49	100.0	1531	8	ADH13197 Human mal
15	49	100.0	1531	8	ADL12474 Human ste
16	49	100.0	1531	8	ADL70599 Cervical
17	49	100.0	1531	8	ADL26776 Human TOP
18	49	100.0	1531	8	ADN03718 Human Antipso
19	49	100.0	1531	8	AAO19281 Human sof
20	49	100.0	1621	4	AA25646 Human pro
21	49	100.0	1626	7	ADJ71211 Human hea
22	49	100.0	1626	7	AAW22646 Type II t
23	49	100.0	1626	7	AAW22646 Type II t
24	49	100.0	1626	7	AAW22646 Type II t
25	49	100.0	1626	7	AAW22646 Type II t

26	37	75.5	82	6	ABM70825 Adm70825 Staphyloc
27	37	75.5	82	6	ABM71532 Adm71532 Staphyloc
28	37	75.5	385	4	ABM58253 Adm58253 Drosophila
29	36	73.5	189	6	AD435435 Ad435435 Acinetoba
30	36	73.5	1665	7	ADP04191 AdP04191 Bacteri
31	35	71.4	219	6	ABU41142 ABU41142 Protein e
32	35	71.4	233	7	ADP04069 AdP04069 Bacteri
33	35	71.4	609	5	ABP26836 ABP26836 Streptoc
34	35	71.4	659	6	ABU19282 ABU19282 Protein e
35	35	71.4	843	6	ABU40604 ABU40604 Protein e
36	35	71.4	855	7	ADP07002 ADP07002 Bacteri
37	34	69.4	88	6	ABM72169 ABM72169 Staphyloc
38	34	69.4	158	4	ABG19995 ABG19995 Novel hum
39	34	69.4	158	4	ABG03180 ABG03180 Novel hum
40	34	69.4	235	2	AAW15763 AAW15763 Cotton fi
41	34	69.4	252	5	ABM48690 ABM48690 Listeria
42	34	69.4	340	4	ABM71784 ABM71784 Drosophila
43	34	69.4	498	4	AAW22646 AAW22646 C glutami
44	34	69.4	569	8	ADK16325 ADK16325 Nanoarcha
45	33	67.3	97	3	AAW48926 AAW48926 Arabidops

ALIGNMENTS

RESULT 1
ABG32304 standard; peptide; 9 AA.
XX
AC ABG32304;
XX
DT 05-NOV-2002 (first entry)
XX
DE HLA-A2 associated immunogenic peptide from human Topoisomerase II.
XX
KW Human; immunogen; epitope; HLA-A1; human leukocyte antigen; CTL;
KW cytotoxic Y lymphocyte; cytotoxic; cancer; colorectal carcinoma;
KW ovarian carcinoma; lung carcinoma; prostate carcinoma; vaccine; tumour;
KW HLA-2; passive immunotherapy; topoisomerase II.
XX
OS Homo sapiens.
XX
PN WO200246416-A2.
XX
PD 13-JUN-2002.
XX
PF 04-DEC-2001; 2001WO-US047290.
XX
PR 04-DEC-2000; 2000US-0251022P.
PR 20-DEC-2000; 2000US-0256824P.
XX
PA (ARGO-) ARGONEX INC.
XX
PI Ramakrishna V, Ross M, Philip R;
XX
DR WPI; 2002-619021/66.
XX
PT New immunogen useful as a vaccine for inducing cytotoxic T-lymphocyte,
PT and for diagnosing, preventing or treating cancer e.g. ovarian carcinoma.
XX
PS Claim 1; Page 50; 60pp; English.
XX
The invention relates to an immunogen comprising an isolated polypeptide
XX whose amino acid sequence comprises an epitopic peptide, does not include
XX MAGE 4 or MAGE-B proteins, or consists of MAGE D protein or its
XX immunologically active fragment. Also included are a polynucleotide
XX encoding the immunogen or its complement, a vector comprising the
XX polynucleotide, a mammalian cell comprising the vector and expressing the
XX polynucleotide, a vaccine composition comprising the immunogen and an
XX antibody specific for the immunogen. The immunogen is useful for inducing
XX a cytotoxic T lymphocyte (CTL) in vitro that is specific for a tumour
XX cell expressing human leukocyte antigen (HLA)-A1 or A2. The immunogen is
XX useful for inducing a CTL response when administered to a subject. A

CC mammalian cell that can express the immunogen, is useful for inducing a
CC CTL response in vitro that is specific for a tumour cell expressing HLA-1
CC or HLA-2. The immunogen or cell is useful for inducing CTL for treating a
CC subject with cancer (carcinoma, preferably colorectal carcinoma, ovarian
CC carcinoma, lung carcinoma and prostate carcinoma). The immunogen is also
CC useful for screening and diagnostic agents, for gene screening in
CC patients afflicted with cancer, for screening a sample for the presence
CC of CTAs that specifically recognise the corresponding epitopes, as a
CC diagnostic tool to evaluate the efficacy of the immunotherapeutic
CC treatments, to prepare class I MHC (major histocompatibility class)
CC tetramers which are utilised in conjunction with flow cytometry to
CC quantitate the frequency of peptide-specific CTL that are present in a
CC sample of lymphocytes from an individual, and for stimulating the
CC production of antibodies for use in passive immunotherapy, for use as
CC diagnostic reagents, and for use as reagents in other processes such as
CC affinity chromatography. The present sequence is an immunogenic epitope
CC of the invention derived from human topoisomerase II

SQ Sequence 9 AA;

Query Match Best Local Similarity 100.0%; Score 49; DB 5; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNQRV 9
|||
Db 1 FLYDDNQRV 9

RESULT 2

ID ABG22395 standard; protein; 546 AA.

AC ABG22395;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22386.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS6582.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 52754; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptides and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 546 AA;

Query Match Best Local Similarity 100.0%; Score 49; DB 4; Length 546;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNQRV 9
|||
Db 261 FLYDDNQRV 269

RESULT 3

ID ABG22397 standard; protein; 1139 AA.

AC ABG22397;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22388.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS6584.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 52756; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (ii) and its binding partners are useful in medical imaging
CC of sites expressing (ii). (i) and (ii) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1139 AA;

Query Match 100.0%; Score 49; DB 4; Length 1139;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 352 FLYDDNORV 360

RESULT 4
ADE61230
ID ADE61230 standard; protein; 1526 AA.
XX
AC ADE61230;
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P41516, SEQ ID NO 7148.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN W02003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P41516.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 1526 AA;

Query Match 100.0%; Score 49; DB 7; Length 1526;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 826 FLYDDNORV 834

RESULT 5
ADD44993
ID ADD44993 standard; protein; 1526 AA.
XX
AC ADD44993;
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P41516, SEQ ID NO 10424.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN W02003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P41516.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

S0 Sequence 1526 AA;

Query Match 100.0%; Score 49; DB 7; Length 1526;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNQRV 9

Db 826 FLYDDNQRV 834

RESULT 6

ADN95295

ID ADN95295 standard; protein; 1530 AA.

XX ADN95295;

DT 01-JUL-2004 (first entry)

DE Human BRC/LBC-related protein sequence SeqID217.

XX growth; differentiation; blood endothelial cell; BRC;

KM lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;

KM lymphatic growth agent; VEGF-C; VEGF-D; angiogenic; cytostatic;

KM vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;

XX inflammatory disease; cancer metastasis; lymphatic system; human.

XX Homo sapiens.

PN WO2003080640-A1.

PD 02-OCT-2003.

PF 07-MAR-2003; 2003WO-US006900.

PR 07-MAR-2002; 2002US-0363019P.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA LTD.

PI Alftalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

DR WPI; 2003-876899/81.

DR N-PSDB; ADN95296.

XX Example 1, SEQ ID NO 217, 176pp; English.

CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprising contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or

CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
CC composition comprising a lymphatic growth agent selected from VEGF-C or
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC the development of compounds with an antiangiogenic, cytostatic,
CC vasotrophic or antiinflammatory activity or for gene therapy. The method
CC is useful in modulating the growth or differentiation of blood
CC endothelial cells or lymphatic endothelial cells, in treating hereditary
CC lymphoedema, in screening for an endothelial cell disorder or
CC predisposition to the disorder or in monitoring the efficacy or toxicity
CC of a drug on endothelial cells. The agent is useful in manufacturing a
CC medicament for the differential modulation of blood vessel endothelial
CC cell or lymphatic vessel endothelial cell growth or differentiation. The
CC lymphatic growth agent may also be used in manufacturing a medicament for
CC the treatment of hereditary lymphoedema resulting from a mutation in a
CC LEC gene or of other diseases involving the lymphatic vessels, such as
CC various inflammatory diseases and cancer metastasis via the lymphatic
CC system. The present sequence is that of a human LEC/BEC differentially
CC expressed protein which is related to the method of the invention. Note:
CC This sequence does not appear in the specification but was obtained by
CC the indexer using the source data given in table 14 of the specification.

S0 Sequence 1530 AA;

Query Match 100.0%; Score 49; DB 7; Length 1530;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNQRV 9

Db 828 FLYDDNQRV 836

RESULT 7

ABP67994

ID ABP67994 standard; protein; 1531 AA.

XX ABP67994;

DT 13-DEC-2002 (first entry)

DE Human colon cancer related polypeptide SEQ ID NO 2593.

XX Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine.

XX Homo sapiens.

PN WO200258534-A2.

PD 01-AUG-2002.

PF 16-NOV-2001; 2001WO-US043704.

PR 20-NOV-2000; 2000US-0252222P.

PR 06-FEB-2001; 2001US-0267011P.

PR 28-MAR-2001; 2001US-0279670P.

PR 10-JUL-2001; 2001US-0304037P.

PA (CORI-) CORIXA CORP.

PI Stolk JA, Xu J, Chenault RA, Meagher MJ, Secrist H, King GE;

DR WPI; 2002-608400/65.

DR N-PSDB; ABV89274.

CC New isolated tumor colon polynucleotide and polypeptide, useful for the
CC diagnosis, prevention and/or treatment of cancer, in particular colon
CC cancer.

Claim 2; SEQ ID NO 2593; 266pp + Sequence Listing; English.

XX The invention relates to a human colon tumour expressed polynucleotide
CC (I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any of
CC 2600 fully defined nucleotide sequences (ABV8669-ABV8289); (ii)
CC sequences of (i); (iii) at least 20 contiguous residues of (i); (iv)
CC sequences that hybridize to (i), under moderately stringent conditions;
CC (v) sequences having at least 75% or 90% identity to (i); or (vi)
CC degenerate variants of (i). The compositions and methods of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC cancer, particularly colon cancer. (i) can be used in gene therapy and
CC (i) and (ii) are useful in pharmaceutical compositions such as vaccines.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WFO
CC at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1531 AA;
Query Match 100.0%; Score 49; DB 5; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDDNQRV 9
Db 828 FLYDDNQRV 836
RESULT 8
AAOI8890
ID AAOI8890 standard; protein; 1531 AA.
AC AAOI8890;
XX 07-NOV-2002 (first entry)
DT Human ovarian cancer associated protein SEQ ID NO: 347.
DE Human; ovarian cancer; cancer.
KW Homo sapiens.
OS Homo sapiens.
XX US2002076715-A1.
FN 20-JUN-2002.
PD 06-JUN-2001; 2001US-00876889.
PF 23-SEP-1998; 98US-00159320.
PR 08-FEB-1999; 99US-00246429.
PR 16-SEP-1999; 99US-00397787.
XX (BENS/) BENSON D R.
PA (LODE/) LODES M J.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G R.
XX Benson DR, Lodes MJ, Mitcham JL, King GE;
PI WPI; 2002-598720/64.
DR Composition for detecting and treating ovarian cancer, comprises a
XX specific polypeptide, polynucleotide, T cell population, or antigen
XX presenting cell.
XX Example 2; Page 142-145; 188pp; English.
XX The present invention relates to a method of detecting the presence of
XX ovarian cancer in a patient, involving detecting ovarian cancer
XX associated polynucleotides. The method is not only used to detect the
XX presence of cancer, preferably ovarian cancer in a patient, but also is
XX used to stimulate and/or expand T cells specific for an ovarian tumour
XX protein. The sequences can be used in vaccines used to treat cancer. The
XX present sequence is an ovarian cancer associated protein

SQ Sequence 1531 AA;
Query Match 100.0%; Score 49; DB 5; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDDNQRV 9
Db 828 FLYDDNQRV 836
RESULT 9
ABG80433
ID ABG80433 standard; protein; 1531 AA.
AC ABG80433;
XX 29-NOV-2002 (first entry)
DT Anti-human type II DNA topoisomerase alpha monoclonal antibody.
DE Human, type II DNA topoisomerase alpha antibody; antibody.
KW Homo sapiens.
OS Homo sapiens.
XX JP2002191364-A.
PN 09-JUL-2002.
PD 26-DEC-2000; 2000JP-00394675.
PF 26-DEC-2000; 2000JP-00394675.
PR 26-DEC-2000; 2000JP-00394675.
PR (MITU) MITSUBISHI CHEM CORP.
PA N-PSDB; ABS66245.
DR WPI; 2002-594353/64.
DR N-PSDB; ABS66245.
XX Detection or determination of a protein, a fused protein, a DNA, a
XX vector, purification of a target protein, a solid carrier, an epitope
XX peptide, a kit for the detection or determination.
XX Disclosure; Page 20-23; 38pp; Japanese.
XX The invention relates to a target protein fused with a polypeptide having
XX an amino acid sequence containing an epitope of anti-human type II DNA
XX topoisomerase alpha antibody and the DNA encoding it. The sequences can
XX be used in a method for the detection or the determination of a target
XX protein in which the target protein is detected or determined by using
XX the reactivity between the target protein and the above fused protein as
XX the index, and also in a method for the purification of a target protein
XX in which the above fused protein is contacted to anti-human type II DNA
XX topoisomerase alpha antibody carried on a solid carrier. This sequence
XX represents an anti-human type II DNA topoisomerase alpha monoclonal
XX antibody
SQ Sequence 1531 AA;
Query Match 100.0%; Score 49; DB 5; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDDNQRV 9
Db 828 FLYDDNQRV 836
RESULT 10
ABU56492
ID ABU56492 standard; protein; 1531 AA.
AC ABU56492;
XX

DT 02-APR-2003 (first entry)
XX Lung cancer-associated polypeptide #85.
DE
XX
XX Lung cancer-associated polypeptide; cytosol; emphysema;
KM antiinflammatory; antistatic; non-small cell lung cancer; atelectasis;
KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
OS
XX
PN WO200286443-A2.
XX
XX 31-OCT-2002.
PD
XX
PF 18-APR-2002; 2002WO-US012476.
XX
XX 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
PI WPI; 2003-093161/08.
DR N-PSDB; ABX76216.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX Claim 27; Page 255; 453pp; English.
PS
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hyperresponsivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention.
XX
XX Sequence 1531 AA;
SQ
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDDNORV 9
DB 828 FLYDDNORV 836
XX
XX RESULT 11
ABR92156 standard; protein; 1531 AA.
ID ABR92156

XX ABR92156;
AC
XX
XX 10-SEP-2003 (first entry)
DT
XX
XX Human cervical cancer cell marker protein SEQ ID NO:222.
DE
XX
XX Human cervical cancer; cervical cancer marker; cancer therapy;
KM detection; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX
PN WO2002101075-A2.
XX
XX 19-DEC-2002.
PD
XX
PF 12-JUN-2002; 2002WO-US018638.
XX
XX 13-JUN-2001; 2001US-0298155P.
PR 13-JUN-2001; 2001US-0298159P.
PR 14-NOV-2001; 2001US-0335936P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
PI Gannavarapu M, Glat K, Hoersch S;
PI WPI; 2003-156967/15.
DR N-PSDB; ACF12939.
XX
XX New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
XX Claim 4; Page 372-376; 386pp; English.
PS
XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (1)
CC given in ABR92047 to ABR92164. A higher level of expression of (1) than
CC normal indicates the presence of cervical cancer. Also described: (1) a
CC vector (II) containing (1); (2) a host cell (III) containing (II); and (3)
CC assessing (W1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (1) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (1) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (1) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX
XX Sequence 1531 AA;
SQ
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDDNORV 9
DB 828 FLYDDNORV 836
XX
XX RESULT 12
ADD44995 standard; protein; 1531 AA.
ID ADD44995
AC ADD44995;
XX
XX 29-JAN-2004 (first entry)
DT
XX Human Protein P11388, SEQ ID NO 10426.
DE
XX

Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.

Homo sapiens.

WO2003016475-A2.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.

(GENO) GEN HOSPITAL CORP.
(FARB) BAYER AG.

Woolf C, D'urso D, Befort K, Costigan M;
WPI; 2003-268312/26.
GENBANK; P11388.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antihoddes. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 1531 AA;

Query Match	100.0%	Score 49;	DB 7;	Length 1531;
Best Local Similarity	100.0%	Pred. No. 2;		
Matches	9;	Conservative	0;	Mismatches 0;
	Indels	0;	Gaps	0;

1 FLYDDNORV 9
|||||||

828 FLYDDNORV 836

RESULT 13
ADE61232
ID ADE61232 standard; protein; 1531 AA.
XX ADE61232;
AC

```

XX 29-JAN-2004 (first entry)
DT
XX
XX Human Protein P11388, SEQ ID NO 7150.
DE
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
PN WO2003016475-A2.
PP
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002WO-US025765.
PR
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX (FARB ) BAYER AG.
PA
XX
XX Woolf C, D'urso D, Belfort K, Costigan M;
PI
XX WPI; 2003-268312/26.
DR GENBANK; P11388.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
XX injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1531 AA.

```



```

RESULT 14
ADH13197
XX ADH13197 standard; protein; 1531 AA.
XX
XX ADH13197,
XX
XX 11-MAR-2004 (first entry)
XX
XX Human malignant neoplasia-related protein Segid46.
XX
XX malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
XX gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
XX bladder cancer; non-small cell lung cancer; human.
XX
XX Homo sapiens.
XX
XX EPI365034-A2.
XX
XX 26-NOV-2003.
XX
XX 09-MAY-2003; 2003EP-00010447.
XX
XX 21-MAY-2002; 2002EP-00010291.
XX 13-FEB-2003; 2003EP-00003112.
XX
XX (FARB ) BAYER AG.
XX
XX Wirtz R, Munnes M, Kallabis H;
XX
XX WPI; 2004-073279/08.
XX
XX N-PSDB; ADH13171.
XX
XX Predicting, diagnosing or prognosing malignant neoplasia by detecting at
XX least two markers, where the markers are genes from one or more
XX chromosomal regions altered in malignant neoplasia,.
XX
XX Claim 12; SEQ ID NO 46; 267bp; English.
XX
XX This invention relates to a novel method for the prediction, diagnosis,
XX or prognosis of malignant neoplasia by the detection of at least two
XX markers. The invention may also be useful for the development of a
XX cytostatic compound through the regulation of the expression of a gene
XX or activity of a protein associated with malignant neoplasia. The method
XX is useful for prediction, diagnosis or prognosis of malignant neoplasia
XX such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
XX oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
XX lung cancer. The polynucleotides and polypeptides defined in the
XX specification, antisense polynucleotides targeting the polynucleotides,
XX antibodies targeting either one of the polynucleotides or polypeptides,
XX and compounds identified by the screening methods are useful for
XX preventing or treating malignant neoplasia. The disease treated is
XX preferably breast cancer. The present sequence is that of a human
XX malignant neoplasia-related protein which may be used in the method of
XX the invention.
XX
XX Sequence 1531 AA;
XX
XX Query Match          100.0%; Score 49; DB 8; Length 1531;
XX Best Local Similarity 100.0%; Pred. No. 2;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 FLYDDNQRV 9
XX |||||
XX 828 FLYDDNQRV 836
XX
XX RESULT 15
XX ADL12474
XX ID ADL12474 standard; protein; 1531 AA.
XX
XX ADL12474,
XX
XX 06-MAY-2004 (first entry)

```

```

XX
XX Human steroid-induced C3A liver cell protein #27.
XX
XX Hepatotropic; Gene therapy; Wilson disease; liver disorder;
XX steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
XX
XX Homo sapiens.
XX
XX US6673549-B1.
XX
XX 06-JAN-2004.
XX
XX 12-OCT-2001; 2001US-00976594.
XX
XX 12-OCT-2000; 2000US-0240409P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Furness LM, Buchbinder JL;
XX
XX WPI; 2004-068610/07.
XX
XX Combination useful for preparing a composition for treating liver
XX disorders associated with steroid therapy, e.g., cirrhosis or hepatitis,
XX comprises cDNAs that are differentially expressed in response to steroid
XX treatment.
XX
XX Disclosure; SEQ ID NO 203; 141bp; English.
XX
XX The invention relates to a combination comprising cDNAs that are
XX differentially expressed in response to steroid treatment. Also included
XX are the following: a high throughput method for using a cDNA to detect
XX differential expression of nucleic acids in a sample; and a high
XX throughput method of screening molecules or compounds to identify a
XX ligand that specifically binds a cDNA. The sample is from a subject with
XX Wilson disease and comparison of a standard defines a stage of that
XX disease. The high throughput method of screening molecules or compounds
XX to identify a ligand that specifically binds a cDNA comprises: combining
XX the combination with molecules or compounds under conditions to allow
XX specific binding; and detecting specific binding between each cDNA and at
XX least one molecule or compound. The molecules or compounds are regulatory
XX proteins. The combination is useful for preparing a composition for
XX treating liver disorders associated with steroid therapy, e.g., cirrhosis
XX or hepatitis. The present sequence represents a human protein which is
XX differentially expressed in steroid-induced C3A liver cells. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1531 AA;
XX
XX Query Match          100.0%; Score 49; DB 8; Length 1531;
XX Best Local Similarity 100.0%; Pred. No. 2;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 FLYDDNQRV 9
XX |||||
XX 828 FLYDDNQRV 836
XX
XX Search completed: December 29, 2004, 16:27:17
XX Job time : 155 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 16:22:15 ; Search time 38 seconds

(without alignments)
15.707 Million cell updates/sec

Title: US-10-006-177-4

Perfect score: 49
Sequence: 1 FLYDDNQRV 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	1531	4	US-09-976-594-203
2	43	87.8	142	1	US-08-470-179-30
3	37	75.5	324	4	US-09-270-767-43224
4	36	73.5	189	4	US-09-328-352-6722
5	36	73.5	1665	4	US-09-543-681A-4476
6	35	71.4	233	4	US-09-543-681A-4354
7	35	71.4	855	4	US-09-543-681A-7287
8	34	69.4	235	2	US-08-580-545B-10
9	34	69.4	235	4	US-09-263-653A-10
10	34	69.4	457	4	US-09-248-796A-23295
11	33	67.3	64	2	US-08-765-179B-19
12	33	67.3	108	1	US-08-259-372A-10
13	33	67.3	108	1	US-08-468-671-10
14	33	67.3	108	4	US-09-025-769B-20
15	33	67.3	108	4	US-09-025-769B-20
16	33	67.3	108	4	US-09-490-070A-20
17	33	67.3	108	4	US-09-490-153-20
18	33	67.3	109	3	US-09-157-370-5
19	33	67.3	113	4	US-09-377-285B-65
20	33	67.3	130	4	US-09-270-767-61055
21	33	67.3	522	3	US-08-894-818B-3
22	33	67.3	522	3	US-09-445-472-4
23	33	67.3	522	4	US-10-090-624-4
24	33	67.3	654	4	US-08-894-818B-35
25	33	67.3	654	3	US-09-445-472-16
26	33	67.3	684	4	US-10-090-624-16
27	33	67.3	715	4	US-09-823-240A-9
					US-09-252-991A-27965

28	33	67.3	902	1	US-08-701-846-2	Sequence 2, Appli
29	32	65.3	109	3	US-09-025-769B-32	Sequence 32, Appl
30	32	65.3	109	3	US-09-025-769B-51	Sequence 51, Appl
31	32	65.3	109	4	US-09-490-070A-32	Sequence 32, Appl
32	32	65.3	109	4	US-09-490-070A-51	Sequence 51, Appl
33	32	65.3	109	4	US-09-490-153-32	Sequence 32, Appl
34	32	65.3	109	4	US-09-490-153-51	Sequence 51, Appl
35	32	65.3	234	4	US-09-372-425A-4	Sequence 4, Appli
36	32	65.3	242	3	US-08-884-569A-5	Sequence 5, Appli
37	32	65.3	286	4	US-09-489-039A-10682	Sequence 10682, A
38	32	65.3	304	4	US-09-248-796A-16060	Sequence 16060, A
39	32	65.3	329	4	US-09-248-796A-14544	Sequence 14544, A
40	32	65.3	358	4	US-09-248-796A-17909	Sequence 17909, A
41	32	65.3	1584	3	US-09-251-645-6	Sequence 6, Appli
42	31.5	64.3	254	4	US-09-266-965-123	Sequence 123, App
43	31	63.3	99	4	US-09-107-532A-5802	Sequence 5802, Ap
44	31	63.3	112	2	US-08-665-202-39	Sequence 39, Appl
45	31	63.3	112	4	US-09-315-574-39	Sequence 39, Appl

ALIGNMENTS

```

RESULT 1
US-09-976-594-203
: Sequence 203, Application US/09976594
: Patent No. 6673549
: GENERAL INFORMATION:
: APPLICANT: Furness, Michael
: TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
: FILE REFERENCE: PA-0041 US
: CURRENT APPLICATION NUMBER: US/09/976,594
: PRIOR FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: 60/240,409
: NUMBER OF SEQ ID NOS: 1143
: SOFTWARE: PERL Program
: SEQ ID NO 203
: LENGTH: 1531
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. 6673549 1867417CD1
US-09-976-594-203

Query Match          100.0%; Score 49; DB 4; Length 1531;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLYDDNQRV 9
      |||||
      828 FLYDDNQRV 836

RESULT 2
US-08-470-179-30
: Sequence 30, Application US/08470179
: Patent No. 5645994
: GENERAL INFORMATION:
: APPLICANT: Huang Ph.D. Wei Mun
: TITLE OF INVENTION: Method and Compositions for
: TITLE OF INVENTION: Identification of Species in a Sample
: NUMBER OF SEQUENCES: 207
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Traak, Britc and Rosaa
: STREET: P.O. Box 2550
: CITY: Salt Lake City
: STATE: Utah
: COUNTRY: USA
: ZIP: 84110
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470.179
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert Ph.D. Susan E.
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801-532-1922
TELEFAX: 801-531-9168
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens sapiens
US-08-470-179-30

Query Match 87.8%; Score 43; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYDNDNRV 9
DB 110 FLYDNDNRV 117

RESULT 3
US-09-270-767-43224
Sequence 43224, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270.767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43224
LENGTH: 324
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-43224

Query Match 75.5%; Score 37; DB 4; Length 324;
Best Local Similarity 77.8%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDNDNRV 9
DB 59 FLYDNDNRV 67

RESULT 4
US-09-328-352-6722
Sequence 6722, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Bretton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328.352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6722
LENGTH: 189
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6722

Query Match 73.5%; Score 36; DB 4; Length 189;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YPDNDNRV 9
DB 108 YPDNDNRV 114

RESULT 5
US-09-543-681A-4476
Sequence 4476, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4476
LENGTH: 1665
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4476

Query Match 73.5%; Score 36; DB 4; Length 1665;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDNDNRV 9
DB 723 FLYDNDNRV 731

RESULT 6
US-09-543-681A-4354
Sequence 4354, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4354
LENGTH: 233
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4354

Query Match 71.4%; Score 35; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDNDNRV 8

Db 45 FVYDDNLR 52

RESULT 7

US-09-543-681A-7287
; Sequence 7287, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7287
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7287

Query Match 71.4%; Score 35; DB 4; Length 855;
Best Local Similarity 62.5%; Pred. No. 2,1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNOR 8
DB 487 YLYEDNOK 494

RESULT 8

US-08-580-545B-10
; Sequence 10, Application US/08580545B
; Patent No. 5932713
; GENERAL INFORMATION:
; APPLICANT: Yoshihisa, Kaaukabe
; APPLICANT: Koichi, Fujisawa
; APPLICANT: Susumu, Nishiguchi
; APPLICANT: Yoshiko, Maekawa
; APPLICANT: Randy, Allen
; TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 601 Thirteenth Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,545B
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bretschneider, Barry E.
; REGISTRATION NUMBER: 28,055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/783-5070
; TELEFAX: 202/783-2331
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-580-545B-10

Query Match 69.4%; Score 34; DB 2; Length 235;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNOR 8
DB 121 FVYENOR 128

RESULT 9

US-09-262-653A-10
; Sequence 10, Application US/09262653A
; Patent No. 6166294
; GENERAL INFORMATION:
; APPLICANT: Yoshihisa, Kaaukabe
; APPLICANT: Koichi, Fujisawa
; APPLICANT: Susumu, Nishiguchi
; APPLICANT: Yoshiko, Maekawa
; APPLICANT: Randy, Allen
; TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 601 Thirteenth Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,653A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bretschneider, Barry E.
; REGISTRATION NUMBER: 28,055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/783-5070
; TELEFAX: 202/783-2331
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-262-653A-10

Query Match 69.4%; Score 34; DB 3; Length 235;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNOR 8
DB 121 FVYENOR 128

RESULT 10

US-09-248-796A-23295
; Sequence 23295, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132

;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 23295
;; LENGTH: 457
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-23295

Query Match 69.4%; Score 34; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYDDNQ 7
Db 162 LYDDNQ 167

RESULT 11
US-08-765-179B-19
;; Sequence 19, Application US/08765179B
;; Patent No. 5854027
;; GENERAL INFORMATION:
;; APPLICANT: STEIRPE, Boris
;; APPLICANT: STEINBACHER, Stefan
;; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
;; TITLE OF INVENTION: OF ANTIBODIES
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
;; STREET: 655 Fifteenth Street N.W. Suite 330
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005-5701
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/765,179B
;; FILING DATE: 14-JAN-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/EP95/02626
;; FILING DATE: 06-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE P 44 25 115.7
;; FILING DATE: 15-JUL-1994
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 64 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-765-179B-19

Query Match 67.3%; Score 33; DB 2; Length 64;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYDDNR 8
Db 17 LYDDNR 23

RESULT 12

US-08-259-372A-10
;; Sequence 10, Application US/08259372A
;; Patent No. 5565354
;; GENERAL INFORMATION:
;; APPLICANT: Osberg, Lars G.
;; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
;; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/259,372A
;; FILING DATE: 14-JUN-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/871,426
;; FILING DATE: 21-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/676,036
;; FILING DATE: 27-MAR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/538,796
;; FILING DATE: 15-JUN-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/192,754
;; FILING DATE: 11-MAY-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 06/925,196
;; FILING DATE: 31-OCT-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 06/904,517
;; FILING DATE: 05-SEP-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-50-7
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-259-372A-10

Query Match 67.3%; Score 33; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYDDNR 8
Db 47 LYDDNR 53

RESULT 13
US-08-468-671-10
;; Sequence 10, Application US/08468671
;; Patent No. 5648077
;; GENERAL INFORMATION:
;; APPLICANT: Osberg, Lars G.
;; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William W.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-671-10

Query Match 67.3%; Score 33; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYDNR 8
:||||:
Db 47 VYDNR 53

RESULT 14
US-09-025-769B-20
Sequence 20, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhann, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-20

Query Match 67.3%; Score 33; DB 3; Length 108;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYDNR 8
:||||:
Db 46 IYDNR 52

RESULT 15
US-09-490-070A-20
Sequence 20, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhann, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A

;
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-490-070A-20

Query Match 67.3%; Score 33; DB 4; Length 108;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYDDNOR 8
:||||:
Db 46 IYDDNKR 52

Search completed: December 29, 2004, 16:31:56
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 16:13:44 ; Search time 188 Seconds

(without alignments)
27,545 Million cell updates/sec

Title: US-10-006-177-4

Perfect score: 49

Sequence: 1 FLYDNDQRV 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	49	100.0	214 2	063176 rattus norv
2	49	100.0	214 2	063177 rattus norv
3	49	100.0	373 2	Q6R6M6 homo sapien
4	49	100.0	373 2	AAR16193 homo sapi
5	49	100.0	1028 2	Q8CCE5 mus musculu
6	49	100.0	1526 1	TP2A CRIGR
7	49	100.0	1526 1	TP2A RAT
8	49	100.0	1526 2	OS5078 cricetulus
9	49	100.0	1526 2	OS5079 cricetulus
10	49	100.0	1528 1	TP2A MOUSE
11	49	100.0	1531 1	TP2A_HUMAN
12	49	100.0	1533 1	TP2A_PIG
13	49	100.0	1553 1	TP2A CHICK
14	49	100.0	1586 2	Q9DFE7
15	49	100.0	1598 2	Q71UH4
16	49	100.0	1598 2	AACT7432
17	49	100.0	1612 1	TP2B CRIO
18	49	100.0	1612 1	TP2B MOUSE
19	49	100.0	1612 2	Q7T0G4
20	49	100.0	1626 1	TP2B_HUMAN
21	49	100.0	1627 1	TP2B CHICK
22	49	89.8	1132 2	Q7ZXS2
23	44	89.8	1579 2	Q6INT0
24	44	89.8	1579 2	AAH72193
25	41	83.7	558 2	Q8Y714
26	41	83.7	558 2	Q720C9
27	41	83.7	558 2	AAT04085
28	40	81.6	644 2	Q9N4W3
29	40	81.6	819 2	Q27537
30	40	81.6	1520 1	TOP2 CAEBL
31	39	79.6	511 2	Q7R8R3

32	38	77.6	1095 2	Q7RSJ8	Q7RSJ8 plasmodium
33	37	75.5	67 2	Q6Z8R4	Q6Z8R4 oryza sativ
34	37	75.5	67 2	BAD10035	BAD10035 oryza sat
35	37	75.5	80 2	Q80089	Q80089 staphylococ
36	37	75.5	80 2	Q6R830	Q6R830 bacteriopho
37	37	75.5	80 2	Q9B0F4	Q9B0F4 staphylococ
38	37	75.5	80 2	Q6GAN4	Q6GAN4 staphylococ
39	37	75.5	80 2	Q6GPF6	Q6GPF6 staphylococ
40	37	75.5	80 2	Q6GCM4	Q6GCM4 staphylococ
41	37	75.5	80 2	Q8NMH8	Q8NMH8 staphylococ
42	37	75.5	80 2	Q931K8	Q931K8 staphylococ
43	37	75.5	80 2	AAR87916	AAR87916 bacteriop
44	37	75.5	82 2	Q9MBR3	Q9MBR3 staphylococ
45	37	75.5	82 2	Q8SDL7	Q8SDL7 staphylococ

ALIGNMENTS

RESULT 1				
ID	Q63176	PRELIMINARY;	PRT;	214 AA.
AC	Q63176;			
DT	01-NOV-1996 (TREMURel. 01, Created)			
DT	01-NOV-1996 (TREMURel. 01, Last sequence update)			
DT	01-OCT-2003 (TREMURel. 25, Last annotation update)			
DE	'DNA topoisomerase IIA' (Fragment).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;			
RX	MEBLINB=93366832; PubMed=8395528;			
RA	Teutsei K., Teutsei K., Okada S., Watanabe M., Shohmori T., Seki S.,			
RA	Inoue Y.;			
RT	"Molecular cloning of partial cDNAs for rat DNA topoisomerase II			
RT	isoforms and their differential expression in brain development."			
RL	J. Biol. Chem. 268:19076-19083 (1993).			
DR	EMBL; D14045; BAA03132.1; -			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0003918; F:DNA binding; IEA.			
DR	GO; GO:0003677; F:DNA binding; IEA.			
DR	GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.			
DR	GO; GO:0016853; F:Isomerase activity; IEA.			
DR	GO; GO:0006265; P:DNA topological change; IEA.			
DR	InterPro; IPR002205; DNA_topoisom.			
DR	Pfam; PF00521; DNA_topoisomIV; 1.			
DR	ProDom; PD000742; DNA_topoisomIV; 1.			
DR	SMART; SM00434; TOPAc; 1.			
KW	Isomerase.			
FT	NON TER			
FT	NON TER			
SO	SEQUENCE	214 AA;	24172 MW;	46A28A1DEA18A5A CRC64;
Query Match				
Best Local Similarity 100.0%; Score 49; DB 2; Length 214;				
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1	FLYDNDQRV 9		
Db	84	FLYDNDQRV 92		
RESULT 2				
ID	Q63177	PRELIMINARY;	PRT;	214 AA.
AC	Q63177;			
DT	01-NOV-1996 (TREMURel. 01, Created)			
DT	01-NOV-1996 (TREMURel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMURel. 26, Last annotation update)			
DE	'DNA topoisomerase IIB' (Fragment).			
OS	Rattus norvegicus (Rat).			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=9336883; PubMed=839528;
RA Teutsui K., Teutsui K., Okada S., Watanabe M., Shohmori T., Seki S.,
RA Inoue Y.;
RT "Molecular cloning of partial cDNAs for rat DNA topoisomerase II
isoforms and their differential expression in brain development."
RL U. Biol. Chem. 268:19076-19083(1993).
DR EMBL; D14046; BA03133.1; -.
DR PIR; B48536; B48536.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR002205; DNA_topoisomI; IEA.
DR Pfam; PF00521; DNA_topoisomI; 1.
DR Prodom; PD000742; DNA_topoisomI; 1.
DR SMART; SM00434; TOP4c; 1.
KW isomerase.
FT NON_TER
FT NON_TER
SQ SEQUENCE 214 AA; 23985 MW; 1FA560E0038C9384 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 84 FLYDDNORV 92

RESULT 3
Q6M6M6

AC 06M6M6; PRELIMINARY; PRT; 373 AA.
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Antigen MAA-44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Chen G., Zhang W.G., Fu J., Cao X.M., Chen Y.X., Zhao W.H., Zhao A.Z.,
RA Han Y.H., Li F.Y., Liu X.P., Yao L.B.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY09240; AAR16193.1; -.
DR InterPro; IPR002205; DNA_topoisomI; IEA.
DR Pfam; PF00521; DNA_topoisomI; 1.
DR Prodom; PD000742; DNA_topoisomI; 1.
DR SMART; SM00434; TOP4c; 1.
SQ SEQUENCE 373 AA; 42817 MW; 95D9F15FB14CCA7B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 7 FLYDDNORV 15

RESULT 4
AAR16193 PRELIMINARY; PRT; 373 AA.

AC AAR16193;
DT 01-APR-2004 (TrEMBLrel. 27, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Antigen MAA-44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Chen G., Zhang W.G., Fu J., Cao X.M., Chen Y.X., Zhao W.H., Zhao A.Z.,
RA Han Y.H., Li F.Y., Liu X.P., Yao L.B.;
RT "Serological identification of immunogenic antigens in acute monocytic leukemia."
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY09240; AAR16193.1; -.
SQ SEQUENCE 373 AA; 42817 MW; 95D9F15FB14CCA7B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 7 FLYDDNORV 15

RESULT 5
Q8CCES
ID 08CCES; PRELIMINARY; PRT; 1028 AA.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 15 days embryo male testis cDNA, RIKEN full-length
DE enriched library, clone:8030493508 product:topoisomerase (DNA) II
DE alpha, full insert sequence. (Fragment).
GN Name=Top2a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcription Research Group Phase I & II Team;
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2049374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630 (2000).

RL [5] SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Testis;

RC MEDLINE=20530913; PubMed=11076861;

RA Shihara K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,

RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,

RA Yoneda Y., Ishikawa T., Tanaka K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771 (2000).

RL [6] SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Testis;

RC Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori P., Imomachi K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishii K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Takawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Control of topological states of DNA by transient

CC breakage and subsequent rejoining of DNA strands. Topoisomerase II

CC makes double-strand breaks (By similarity).

CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining

CC of double-stranded DNA.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both

CC negative and positive supercoils, whereas prokaryotic enzymes

CC relax only negative supercoils (By similarity).

CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

DR EMBL; AK033321; BAC28232.1; -.

DR MGD; MG1:98790; Top2a.

DR GO; GO:0000793; C:condensed chromosome; IDA.

DR GO; GO:0005730; C:nucleolus; IDA.

DR GO; GO:0030261; P:chromosome condensation; IMP.

DR GO; GO:0007059; P:chromosome segregation; IMP.

DR GO; GO:0040016; P:embryonic cleavage; IMP.

DR InterPro; IPR003957; CBF_A_NFYB_topis.

DR InterPro; IPR01558; DNA_GYRase_B.

DR InterPro; IPR001241; DNA_topoisom.

DR InterPro; IPR002203; DNA_topoisom.

DR Pfam; PF00521; DNA_topoisom.

DR PRINTS; PR00615; CCAATSUBUNITA.

DR PRINTS; PR00418; TP12FAMILY.

DR PRODOM; PD000742; DNA_topoisom.

DR PRODOM; PD000742; DNA_topoisom.

DR SMART; SM00433; TOP2c; 1.

DR SMART; SM00434; TOP2c; 1.

DR SMART; SM00434; TOP2c; 1.

DR ATP-binding; DNA-binding; Isomerase; Topoisomerase.

DR ATP-binding; DNA-binding; Isomerase; Topoisomerase.

FT NON TER 1 1

FT SEQUENCE 1028 AA; 116484 MW; A0ACD911B39367CD CRC64;

Query Match 100.0%; Score 49; DB 2; Length 1028;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNQRV 9

Db 328 FLYDDNQRV 336

TP2A CRIGR STANDARD; PRT; 1526 AA.

AC PA1515;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).

GN Name=TOP2A; Synonyms=TOP2, TOP-2;

OS Cricetulus ginseng (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Cricetulus.

OX NCBI_TaxID=10029;

XM [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=93131977; PubMed=8380592;

RA Chan V.T., Ng S.W., Eder J.P., Schnipper L.E.;

RT "Molecular cloning and identification of a point mutation in the

RT topoisomerase II cDNA from an ecoposide-resistant Chinese hamster

RT ovary cell line.";

RL J. Biol. Chem. 268:2160-2165 (1993).

CC -1- FUNCTION: Control of topological states of DNA by transient

CC breakage and subsequent rejoining of DNA strands. Topoisomerase II

CC makes double-strand breaks.

CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining

CC of double-stranded DNA.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both

CC negative and positive supercoils, whereas prokaryotic enzymes

CC relax only negative supercoils.

CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

CC -----

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DR EMBL; L04607; AAA37023.1; -.

DR PIR; A44406; A44406.

DR HSSP; P06786; 1BTT.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR003957; CBF_A_NFYB_topis.

DR InterPro; IPR001241; DNA_topoisom.

DR InterPro; IPR002203; DNA_topoisom.

DR Pfam; PF00204; DNA_GYRaseB; 1.

DR Pfam; PF00521; DNA_topoisom.

DR Pfam; PF02518; HATPase_C; 1.

DR PRINTS; PR00615; CCAATSUBUNITA.

DR PRINTS; PR00418; TP12FAMILY.

DR PRODOM; PD000742; DNA_topoisom.

DR PRODOM; PD000742; DNA_topoisom.

DR SMART; SM00387; HATPase_C; 1.

DR SMART; SM00433; TOP2c; 1.

DR SMART; SM00434; TOP2c; 1.

DR PROSITE; PS00177; TOPISOMERASE_II; 1.

DR ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.

FT NP BIND 160 165

FT ACT SITE 804 804

FT VARIANT 493 493

FT SEQUENCE 1526 AA; 173196 MW; 5FB2DBF8F1C02929 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1526;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNQRV 9

Db 827 FLYDDNQRV 835

RESULT 6

TP2A_CRIGR

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RESULT 7
TP2A_RAT
ID TP2A_RAT STANDARD; PRT; 1526 AA.
AC P41516;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3) .
GN Name=Top2a; Synonym=Top2, Top-2;
OS Rattus norvegicus (Rat) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=93290677; PubMed=8390253;
RA Park S.H., Yoon J.H., Kwon Y.D., Park S.D.;
RT "Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase
RT II."
RL Blochem. Biophys. Res. Commun. 193:787-793(1993) .
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC -----
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CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch) .
CC -----
CC EMBL; Z46372; CAAB6496.1; -.
CC EMBL; Z19552; CAA79611.1; -.
CC DR EMBL; Z29676; -; NOT_ANNOTATED_CDS.
CC DR HSSP; P06786; 1BJT.
CC DR RGD; 62048; Top2a.
CC DR InterPro; IPR003594; ATPbind_ATPase.
CC DR InterPro; IPR003957; CERA_NFYB_top1b.
CC DR InterPro; IPR001241; DNA_topoisomII.
CC DR InterPro; IPR002205; DNA_topoisomIV.
CC DR Pfam; PF00204; DNA_gyraseB; 1.
CC DR Pfam; PF00521; DNA_topoisomIV; 1.
CC DR Pfam; PF02518; HATPase_C; 1.
CC DR PRINTS; PR00615; CCAATSUBNTA.
CC DR PRINTS; PR00418; TP12FAMILY.
CC DR ProDom; PD000742; DNA_topoisomIV; 1.
CC DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
CC KW ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.
CC FT NP BIND 159 164 ATP (Potential).
CC FT ACT SITE 803 803 DNA cleavage (by similarity).
CC SQ SEQUENCE 1526 AA; 173220 MW; A1961ABDB1B050F CRC64;

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ID      055078      PRELIMINARY;      PRI;      1526 AA.
AC      01-JUN-1998 (TREMBLRel. 06, Created)
DT      01-JUN-1998 (TREMBLRel. 06, Last sequence update)
DT      01-OCT-2003 (TREMBLRel. 25, Last annotation update)
DE      DNA topoisomerase II alpha (EC 5.99.1.3).
OS      Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Cricetus.
OX      NCBI_TaxID=10030;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RX      MEDLINE=99445695; PubMed=10519406;
RA      Khetlija T., Rene B., Le Mee S., Jacquemin-Sablon J.M.,
RA      Markovits J., Jacquemin-Sablon H., Jacquemin-Sablon A.;
RT      "Transfection of 9-Hydroxyethylpicoline-resistant chinese hamster
RT      fibroblasts with human Topoisomerase IIalpha cDNA selective
RT      restoration of the sensitivity to DNA religation inhibitors.";
RT      Cancer Res. 59:4927-4936 (1999).
RL      -1- FUNCTION: Conflicts of topological states of DNA by transient
CC      breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC      makes double-strand breaks (by similarity).
CC      -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC      of double-stranded DNA.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC      negative and positive supercoils, whereas prokaryotic enzymes
CC      relax only negative supercoils (By similarity).
CC      -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR      EMBL; Y16594; CA67312.1; -.
DR      HSBP; P06786; 1BYT.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR      GO; GO:0006255; P:DNA topological change; IEA.
DR      InterPro; IPR003594; ATPbind_ATPase.
DR      InterPro; IPR003957; CBFA_NFYB_Topis.
DR      InterPro; IPR011558; DNA_gyrase_B.
DR      InterPro; IPR001241; DNA_topoisoi.
DR      InterPro; IPR002205; DNA_topoisolv.
DR      Pfam; PF00204; DNA_gyraseB_1.
DR      Pfam; PF00521; DNA_topoisolv; 1.
DR      Pfam; PF02518; HATPase_c/1.
DR      PRINTS; PR00615; CCAATSUBUNITA.
DR      PRINTS; PR00418; TP12FAMILY.
DR      ProDom; PD149633; DNA_gyrase_B; 1.
DR      ProDom; PD000742; DNA_topoisolv; 1.
DR      SMART; SM00387; HATPase_c/1.
DR      SMART; SM00433; TOP2c; 1.
DR      SMART; SM00434; TOP4c; 1.
DR      PROSITE; PS00177; TOPOISOMERASE II; 1.
KW      ATP-binding; DNA-binding; Isomerase; Topoisomerase.
SEQUENCE 1526 AA; 173156 MW; 9E0CEB68233CBCC CR664;

Query Match      100.0%; Score 49; DB 2; Length 1526;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FLYDNDORV 9
|||||||
827 FLYDNDORV 835

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RESULT 8
055078

RESULT 9	
055079	
ID 055079	PRELIMINARY;
AC 055079:	PRT; 1526 AA.
DT 01-JUN-1998	(TREMBLrel. 06, Created)
DT 01-JUN-1998	(TREMBLrel. 06, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DB DNA topoisomerase II alpha (EC 5.99.1.3).
 OS Citreolus longicaudatus (long-tailed hamster) (Chinese hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Citreolus.
 CC NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Delaporte C., Lambert B., Le Mee S., Chaminade F., Saucier J.M.,
 RA Jacquemont-Sablou A.,
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Control of topological states of DNA by transient
 CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
 CC makes double-strand breaks (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
 CC negative and positive supercoils, whereas prokaryotic enzymes
 CC relax only negative supercoils (By similarity).
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 DR HSSP; P06786; 1BUT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO; GO:0016853; P:isomerase activity; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR003957; CBFA_NFYB_topis.
 DR InterPro; IPR011558; DNA_gyrase_B.
 DR InterPro; IPR01241; DNA_topoisolt.
 DR InterPro; IPR002205; DNA_topoisolt.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisolt; 1.
 DR PRINTS; PR00615; HATPase_c; 1.
 DR PRINTS; PR00418; CCAATSUBUNITA.
 DR PRODOM; PD14963; DNA_gyrase_B; 1.
 DR PRODOM; PD000742; DNA_topoisolt; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR KEGG; K00001; DNA-binding; Isomerase; Topoisomerase.
 DR ATP-binding; DNA-binding; Isomerase; Topoisomerase.
 SO SEQUENCE 1526 AA; 173097 MW; 5E73723C87019929 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 1526;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
 Db 827 FLYDDNORV 835

RESULT 10
 TP2A_MOUSE STANDARD; PRT; 1528 AA.
 AC Q01320;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
 GN Name=Top2a; Synonym=Top2; Top-2;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=93065194; PubMed=1331984;
 RA Adachi N., Miyake M., Ikeda H., Kikuchi A.;
 RT "Characterization of cDNA encoding the mouse DNA topoisomerase II that
 RT can complement the budding yeast top2 mutation.";
 RT Nucleic Acids Res. 20:5297-5303 (1992).
 RN [2]
 RP SEQUENCE OF 1254-1528 FROM N.A.
 RC TISSUE=Lymphoma;
 RX MEDLINE=94084643; PubMed=8261398;
 RA McPherson J., Brown G.A., Goldenberg G.J.;
 RT "Characterization of a DNA topoisomerase IIalpha gene rearrangement in
 RT adriamycin-resistant p38 leukemia: expression of a fusion messenger
 RT RNA transcript encoding topoisomerase IIalpha and the retinoic acid
 RT receptor alpha locus.";
 RL Cancer Res. 53:5885-5889 (1993).
 CC -1- FUNCTION: Control of topological states of DNA by transient
 CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
 CC makes double-strand breaks.
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SUBUNIT: Homodimer.
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
 CC negative and positive supercoils, whereas prokaryotic enzymes
 CC relax only negative supercoils.
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC -----
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DR EMBL; D12513; BA002076.1; -;
 DR EMBL; U01915; AAC52135.1; -;
 DR FTR; JS0703; JS0703.
 DR HSSP; P06786; 1BUT.
 DR MGD; MGI:98790; Top2a.
 DR GO; GO:0000793; C:condensed chromosome; IDA.
 DR GO; GO:0005730; C:nucleolus; IDA.
 DR GO; GO:0030261; P:chromosome condensation; IMP.
 DR GO; GO:0007059; P:chromosome segregation; IMP.
 DR GO; GO:0040016; P:embryonic cleavage; IMP.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR003957; CBFA_NFYB_topis.
 DR InterPro; IPR001241; DNA_topoisolt.
 DR InterPro; IPR002205; DNA_topoisolt.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisolt; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR PRINTS; PR00615; CCAATSUBUNITA.
 DR PRINTS; PR00418; TP12FAMILY.
 DR PRODOM; PD000742; DNA_topoisolt; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR KEGG; K00001; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.
 DR ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.
 FT NP_BIND 160 165 ATP (Potential).
 FT ACT_SITE 804 804 DNA cleavage (By similarity).
 SO SEQUENCE 1528 AA; 172876 MW; 9061778DCA6C756A CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1528;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
 Db 827 FLYDDNORV 835

RESULT 11
ID TP2A_HUMAN STANDARD; PRT: 1531 AA.
AC P11386; Q9HB24; Q9HB25; Q9UP44; Q9UCP9;
DT 01-JUL-1989 (Rel. 11, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
GN Name=TOP2A; Synonyms=TOP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99017161; PubMed=2845399;
RA Tsai-Pflugfelder M., Liu L.F., Liu A.A., Tewey K.M., Whang-Peng J.,
RT Knutsen T., Huebner K., Croce C.M., Wang J.C.;
RT "Cloning and sequencing of cDNA encoding human DNA topoisomerase II
RT and localization of the gene to chromosome region 17q21-22.";
RT Proc. Natl. Acad. Sci. U.S.A. 85:7177-7181(1988).
RN [2]
RP REVISIONS TO 109-114.
RX MEDLINE=93338672; PubMed=8393377;
RA Tsai-Pflugfelder M., Wang J.C.;
RT Unpublished results, cited by:
RL Masserman R.A., Austin C.A., Fisher L.M., Wang J.C.;
RL Cancer Res. 53:3591-3596(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99013880; PubMed=9795238;
RA Lang A.J., Mirskil S.E., Cummings H.J., Yu Q., Gerlach J.H., Cole S.P.;
RT "Structural organization of the human TOP2A and TOP2B genes.";
RL Gene 221:255-266(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99196712; PubMed=10095062; DOI=10.1016/S0167-4781(99)00020-2;
RA Sing J.H., Heaton V.J., Bell M., Mani P., Austin C.A., Fisher L.M.;
RT "Molecular cloning and characterization of the human topoisomerase
RT IIalpha and IIbeta genes: evidence for Isoform evolution through gene
RT duplication.";
RL Biochim. Biophys. Acta 1444:395-406(1999).
RN [5]
RP SEQUENCE OF 1-500 FROM N.A. (ISOFORMS 2; 3 AND 4).
RA Petruti-Mot A.S., Earnshaw W.C.;
RT "Two differentially spliced forms of topoisomerase II alpha and beta
RT mRNA are conserved between birds and humans.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEAR EXPORT SIGNAL.
RX MEDLINE=22705291; PubMed=12821127; DOI=10.1016/S0006-291X(03)01077-5;
RA Mirskil S.E., Bielawski J.C., Cole S.P.;
RT "Identification of functional nuclear export sequences in human
RT topoisomerase IIalpha and beta.";
RL Biochem. Biophys. Res. Commun. 306:905-911(2003).
RN [7]
RP VARIANT AMSACRINE-RESISTANT LYS-487.
RX MEDLINE=9133186; PubMed=1651812;
RA Hinde M., Deisseroth K., Mayes J., Altschuler E., Jansen R.,
RT Ledley F.D., Zweilling L.A.;
RT "Identification of a point mutation in the topoisomerase II gene from
RT a human leukemia cell line containing an amesacrine-resistant form of
RT topoisomerase II.";
RL Cancer Res. 51:4729-4731(1991).
RN [8]
RP VARIANT TENIPOSIDE-RESISTANT GLN-450.
RX MEDLINE=91352047; PubMed=1652758;
RA Bugg B.Y., Danke M.K., Beck W.T., Suttle D.P.;
RT "Expression of a mutant DNA topoisomerase II in CCRF-CEM human
RT leukemic cells selected for resistance to teniposide.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7654-7658(1991).
CC -1- FUNCTION: Control of topological states of DNA by transient

CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- ENZYME REGULATION: Specifically inhibited by the intercalating
CC agent amesacrine.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear; generally located
CC in the nucleoplasm.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P11388-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P11388-2; Sequence=VSP_006531;
CC Name=3;
CC IsoId=P11388-3; Sequence=VSP_006529;
CC Name=4;
CC IsoId=P11388-4; Sequence=VSP_006530;
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04088; AAA61209.1; -;
DR EMBL; AF071747; AAC77388.1; -;
DR EMBL; AF071738; AAC77388.1; JOINED.
DR EMBL; AF071739; AAC77388.1; JOINED.
DR EMBL; AF071740; AAC77388.1; JOINED.
DR EMBL; AF071741; AAC77388.1; JOINED.
DR EMBL; AF071742; AAC77388.1; JOINED.
DR EMBL; AF071743; AAC77388.1; JOINED.
DR EMBL; AF071744; AAC77388.1; JOINED.
DR EMBL; AF071745; AAC77388.1; JOINED.
DR EMBL; AF071746; AAC77388.1; JOINED.
DR EMBL; AF071747; AAC77388.1; JOINED.
DR EMBL; AF071748; AAC77388.1; JOINED.
DR EMBL; AF071749; AAC77388.1; JOINED.
DR EMBL; AF071750; AAC77388.1; JOINED.
DR EMBL; AF071751; AAC77388.1; JOINED.
DR EMBL; AF071752; AAC77388.1; JOINED.
DR EMBL; AF071753; AAC77388.1; JOINED.
DR EMBL; AF071754; AAC77388.1; JOINED.
DR EMBL; AF071755; AAC77388.1; JOINED.
DR EMBL; AF071756; AAC77388.1; JOINED.
DR EMBL; AF071757; AAC77388.1; JOINED.
DR EMBL; AF071758; AAC77388.1; JOINED.
DR EMBL; AF285157; AAC13403.1; -;
DR EMBL; AF285158; AAC13404.1; -;
DR EMBL; AF285159; AAC13405.1; -;
DR PDB; 1WZ; Model; A=431-1252.
DR Genew; HGNC:11989; TOP2A.
DR MIM; 126430; -;
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0003677; F:DNA binding; TAS.
DR GO; GO:0003187; F:DNA topoisomerase (ATP-hydrolyzing) activity; TAS.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003957; CBFA_NFYB_topis.
DR InterPro; IPR001241; DNA_topoisomII.

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DR InterPro: IPR002205; DNA_topoisomIv.
DR Pfam: PF00204; DNA_gyraseB. 1.
DR Pfam: PF00521; DNA_topoisomIv. 1.
DR Pfam: PF02518; HATPase_C. 1.
DR PRINTS: PR00615; CCAATSUBUNTA.
DR PRINTS: PR00418; TP12FAMILY.
DR ProDom: PD000742; DNA_topoisomIv. 1.
DR SMART: SM00387; HATPase_C. 1.
DR SMART: SM00433; TOP2c. 1.
DR SMART: SM00434; TOP2c. 1.
DR PROSITE: PS00177; TOPOISOMERASE II; 1.
DR 3D-structure: Alternative splicing: ATP-binding; DNA-binding;
KW Isomerase; Nuclear protein; Polymorphism; Topoisomerase.
FT NP_BIND 161 166
FT DOMAIN 1018 1028
FT ACT_SITE 805 805
FT VARSPLIC 321 321
FT FT
FT VARSPLIC 355 355
FT FT
FT FT
FT VARSPLIC 401 401
FT FT
FT VARSPLIC 450 450
FT FT
FT VARSPLIC 487 487
FT FT
FT CONFLICT 152 152
FT CONFLICT 180 180
FT CONFLICT 327 327
FT CONFLICT 1022 1022
FT CONFLICT 1274 1274
FT CONFLICT 1295 1295
FT SEQUENCE 1531 AA; 174384 MW; 3DPA0BC9E84789DC CRC64;
SQ
Query Match 100.0%; Score 49; DB 1; Length 1531;
Best Local Similarity 100.0%; Pred. No. 1;8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 FLYDDNGRV 9
DB 828 FLYDDNGRV 836
RESULT 12
TP2A_PIG STANDARD; PRT; 1533 AA.
ID TP2A_PIG
AC 046374;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
DN Name=TOP2A;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid:9823;
RX (1)
RN SEQUENCE FROM N.A.
RP TISSUE=Muscle;
RA Ito Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer.
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both

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CC      negative and positive supercoils, whereas prokaryotic enzymes
CC      relax only negative supercoils.
CC      -I- SIMILARITY: Belongs to the type II topoisomerase family.
CC      -----
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC      -----
CC      EMBL: AB009387; BAA23778.1; -
CC      DR      HSPB, P06786; IBT.
CC      DR      InterPro: IPR003594; ATPbind_ATPase.
CC      DR      InterPro: IPR003957; CBPA_NFYB_topis.
CC      DR      InterPro: IPR001241; DNA_topoisolI.
CC      DR      InterPro: IPR002205; DNA_topoisolv.
CC      DR      Pfam: PF00204; DNA_gyraseB; 1.
CC      DR      Pfam: PF00521; DNA_topoisolv; 1.
CC      DR      Pfam: PF02518; HATPase_c; 1.
CC      DR      PRINTS: PR00615; CCAATSUBUNTA.
CC      DR      PRINTS: PR00418; TP12FAMILY.
CC      DR      Prodom: PD000742; DNA_topoisolv; 1.
CC      DR      SMART; SM00387; HATPase_c; 1.
CC      DR      SMART; SM00433; TOP2c; 1.
CC      DR      SMART; SM00434; TOP4c; 1.
CC      DR      PROSITE; PS00177; TOPISOISOMERASE II; 1.
CC      DR      ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.
CC      FT      NP_BIND 161 166      ATP (Potential).
CC      FT      ACT_SITE 805 805      ATP cleavage (By similarity).
CC      SQ      SEQUENCE 1533 AA; 174306 MW; 529782573BCA6BD2 CRC64;
CC
CC      Query Match          100.0%; Score 49; DB 1; Length 1533;
CC      Best Local Similarity 100.0%; Pred. No. 1,8;
CC      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY      1 FLYDNDGRV 9
CC      Db      828 FLYDNDGRV 836
CC
CC      RESULT 13
CC      ID      TP2A_CHICK STANDARD; PRT; 1553 AA.
CC      AC      042130;
CC      DT      15-JUN-1998 (Rel. 36, Created)
CC      DT      16-OCT-2001 (Rel. 40, Last sequence update)
CC      DT      05-JUN-2004 (Rel. 44, Last annotation update)
CC      DE      DNA topoisomerase II, alpha isozyme (EC 5.99.1.3) .
CC      GN      Name=TOP2A;
CC      OS      Gallus gallus (Chicken) .
CC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC      Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC      OC      Gallus.
CC      OX      NCBI_TaxID=9031;
CC      RN      [1]
CC      RP      SEQUENCE FROM N.A.
CC      RX      MEDLINE=21346110; PubMed=11453553;
CC      RA      "Mimi A., Suka N., Harata M., Kikuchi A., Mizuno S.;"
CC      RT      "Co-localization of chicken DNA topoisomerase IIalpha, but not beta,
CC      RL      with sites of DNA replication and possible involvement of a C-terminal
CC      RL      region of alpha through its binding to PCNA.";
CC      RL      Chromosoma 110:102-114(2001) .
CC      CC      -I- FUNCTION: Control of topological states of DNA by transient
CC      CC      breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC      CC      makes double-strand breaks (By similarity).
CC      CC      -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC      CC      of double-stranded DNA.
CC      CC      -I- SUBUNIT: Homodimer (By similarity).
CC      CC      -I- SUBCELLULAR LOCATION: Nuclear; generally located in the
CC      CC      nucleoplasm.
CC      CC      -I- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both

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CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
-----
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CC EMBL; AB007445; BAA2539.2; -.
CC HSSP; P06786; 1BUT.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR003957; CBFA_NFYB_top1s.
CC InterPro; IPR001241; DNA_topoisomII.
CC InterPro; IPR002205; DNA_topoisomIV.
CC Pfam; PF00204; DNA_gyraseB; 1.
CC Pfam; PF00521; DNA_topoisomIV; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC PRINTS; PR00615; CCAATSUBUNTA.
CC PRINTS; PR00418; TP12FAMILY.
CC ProDom; PD000742; DNA_topoisomIV; 1.
CC SMART; SM00387; HATPase_c; 1.
CC SMART; SM00433; TOP2c; 1.
CC SMART; SM00434; TOP2c; 1.
CC PROSITE; PS00177; TOPOISOMERASE_II; 1.
CC ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.
CC NP_BIND; 162 167 ATP (Potential).
CC FT ACT_SITE; 806 806 DNA cleavage (By similarity).
CC SEQUENCE; 1553 AA; 174991 MW; 3322CE95238F71B2 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1553;
Best Local Similarity 100.0%; Pred. NO. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 829 FLYDDNORV 837

RESULT 14
Q9DPB7 PRELIMINARY; PRT; 1586 AA.
AC Q9DPB7;
ID Q9DPB7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Topoisomerase II alpha-2.
DE Name=TOP2A;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Petruti-Mot A.S., Barnshaw W.C.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AF285155; AAG13401.1; -.
DR HSSP; P06786; 1BUT.
DR GO; GO:0005634; C:nucleus; IEA.

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003957; CBFA_NFYB_top1s.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR002205; DNA_topoisomIV.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00615; CCAATSUBUNTA.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR ProDom; PD000742; DNA_topoisomIV; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00433; TOP2c; 1.
DR SMART; SM00434; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
CC ATP-binding; DNA-binding; Isomerase; Topoisomerase.
CC SEQUENCE; 1586 AA; 178839 MW; 422CF3A60EAB86 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 1586;
Best Local Similarity 100.0%; Pred. NO. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 864 FLYDDNORV 872

RESULT 15
Q71UH4 PRELIMINARY; PRT; 1598 AA.
ID Q71UH4;
AC Q71UH4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DNA topoisomerase II beta (Fragment).
DE Name=TOP2B;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99013880; PubMed=9795238;
RA Lang A.J., Mirek S.E., Cummings H.J., Yu Q., Gerlach J.H., Cole S.P.;
RT "Structural organization of the human TOP2A and TOP2B genes.";
RL Gene 221:255-266 (1998).
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AF087160; AAC77432.1; -.
DR EMBL; AF087143; AAC77432.1; JOINED.
DR EMBL; AF087144; AAC77432.1; JOINED.
DR EMBL; AF087145; AAC77432.1; JOINED.
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DR EMBL; AF087148; AAC77432.1; JOINED.
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DR EMBL; AF087150; AAC77432.1; JOINED.
DR EMBL; AF087151; AAC77432.1; JOINED.
DR EMBL; AF087152; AAC77432.1; JOINED.

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DR EMBL; AF087153; AAC77432.1; JOINED.
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 DR EMBL; AF087158; AAC77432.1; JOINED.
 DR EMBL; AF087159; AAC77432.1; JOINED.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR InterPro; IPR003594; ATPbind ATPase.
 DR InterPro; IPR003597; CBFA_NFYB_topis.
 DR InterPro; IPR011558; DNA_gyrase_B.
 DR InterPro; IPR001241; DNA_topoisolv.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisolv; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PRINTS; PR00418; TP12FAMILY.
 DR Prodom; PD149633; DNA_gyrase_B; 1.
 DR Prodom; PD000742; DNA_topoisolv; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
 DR ATP-binding; DNA-binding; Isomerase; Topoisomerase.
 FT NON_TER 1
 SQ SEQUENCE 1598 AA; 180613 MW; B56467250AB2EB80 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 1598;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDNGRV 9
 |||||
 Db 821 FLYDNGRV 829

Search completed: December 29, 2004, 16:30:29
 Job time : 190 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 16:30:36 ; Search time 144 Seconds

(without alignments)
22.483 Million cell updates/sec

Title: US-10-006-177-4

Perfect score: 49

Sequence: 1 FLYDNDQNV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	14	US-10-006-177-4
2	49	100.0	990	13	US-10-087-192-477
3	49	100.0	1083	13	US-10-087-192-480
4	49	100.0	1526	17	US-10-471-758-2
5	49	100.0	1531	9	US-09-876-889-347
6	49	100.0	1531	9	US-09-998-598-2593
7	49	100.0	1531	14	US-10-171-311-222
8	49	100.0	1531	14	US-10-301-822-211
9	49	100.0	1531	15	US-10-435-596-46
10	49	100.0	1531	17	US-10-723-860-2100
11	49	100.0	1621	15	US-10-296-115-1161
12	49	100.0	1626	16	US-10-408-765A-3017
13	40	81.6	816	14	US-10-369-493-5435

14	40	81.6	1520	14	US-10-369-493-5596	Sequence 5596, Ap
15	40	81.6	1520	14	US-10-369-493-5597	Sequence 5597, Ap
16	37	75.5	250	16	US-10-779-461-11	Sequence 11, Appl
17	37	75.5	251	16	US-10-779-461-51	Sequence 51, Appl
18	37	75.5	617	16	US-10-437-963-162226	Sequence 162226,
19	35	71.4	83	15	US-10-425-114-47619	Sequence 47619, A
20	35	71.4	219	16	US-10-282-122A-69066	Sequence 69066, A
21	35	71.4	274	16	US-10-437-963-109620	Sequence 109620,
22	35	71.4	441	14	US-10-369-493-3569	Sequence 3569, Ap
23	35	71.4	463	17	US-10-425-115-295784	Sequence 295784,
24	35	71.4	618	17	US-10-425-115-347738	Sequence 347738,
25	35	71.4	623	15	US-10-425-114-53896	Sequence 53896, A
26	35	71.4	655	14	US-10-369-493-20595	Sequence 20595, A
27	35	71.4	659	15	US-10-282-122A-47206	Sequence 47206, A
28	35	71.4	693	14	US-10-156-761-9305	Sequence 9305, Ap
29	35	71.4	843	14	US-10-282-122A-68528	Sequence 68528, A
30	35	71.4	2122	16	US-10-437-963-189782	Sequence 189782,
31	34	69.4	78	15	US-10-424-599-182919	Sequence 182919,
32	34	69.4	223	16	US-10-767-701-35086	Sequence 35086, A
33	34	69.4	223	17	US-10-425-115-284417	Sequence 284417,
34	34	69.4	388	17	US-10-425-115-351465	Sequence 351465,
35	34	69.4	463	17	US-10-425-115-351466	Sequence 351466,
36	34	69.4	498	9	US-09-738-626-6678	Sequence 6678, Ap
37	34	69.4	545	17	US-10-739-930-10196	Sequence 10196, A
38	34	69.4	902	16	US-10-437-963-116905	Sequence 116905,
39	34	69.4	967	16	US-10-437-963-118888	Sequence 118888,
40	34	69.4	1011	16	US-10-437-963-117329	Sequence 117329,
41	34	69.4	2364	14	US-10-156-761-7834	Sequence 7834, Ap
42	33	67.3	63	16	US-10-767-701-48543	Sequence 48543, A
43	33	67.3	98	14	US-10-308-817-117	Sequence 117, Ap
44	33	67.3	98	15	US-10-453-698-117	Sequence 117, Ap
45	33	67.3	103	10	US-09-972-656-130	Sequence 130, Ap

ALIGNMENTS

RESULT 1
US-10-006-177-4
Sequence 4, Application US/10006177
Publication No. US2003016551A1
GENERAL INFORMATION:
APPLICANT: Ramakrishna, Venky
APPLICANT: Ross, Mark
TITLE OF INVENTION: Cytotoxic T-Lymphocyte-Inducing Immunogens for Prevention, Treat
FILE REFERENCE: 26747-35
CURRENT FILING DATE: 2001-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US/60/251,022
PRIOR FILING DATE: 2000-12-04
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Epitopic Peptide
US-10-006-177-4

Query Match 100.0%; Score 49; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDNDQNV 9
|||||||
Db 1 FLYDNDQNV 9

RESULT 2
US-10-087-192-477
; Sequence 477, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 990
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-477

Query Match 100.0%; Score 49; DB 13; Length 990;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNORV 9
Db 289 FLYDDNORV 297

RESULT 3
US-10-087-192-480
; Sequence 480, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-480

Query Match 100.0%; Score 49; DB 13; Length 1083;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNORV 9
Db 671 FLYDDNORV 679

RESULT 4
US-10-471-758-2
; Sequence 2, Application US/10471758
; Publication No. US20040249574A1
; GENERAL INFORMATION:
; APPLICANT: Tiebby, Natcail
; APPLICANT: Seidlin, Yevgeny

; APPLICANT: Bejerano, Gali
; APPLICANT: Margalit, Hanah
; TITLE OF INVENTION: Markovian Domain Fingerprinting In Statistical Segmentation Of
; TITLE OF INVENTION: Protein Sequences
; FILE REFERENCE: 26874
; CURRENT APPLICATION NUMBER: US/10/471,758
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1526
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-10-471-758-2

Query Match 100.0%; Score 49; DB 17; Length 1526;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNORV 9
Db 827 FLYDDNORV 835

RESULT 5
US-09-876-889-347
; Sequence 347, Application US/09876889
; Patent No. US20020076715A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Kling, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.466C3
; CURRENT APPLICATION NUMBER: US/09/876,889
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-889-347

Query Match 100.0%; Score 49; DB 9; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLYDDNORV 9
Db 828 FLYDDNORV 836

RESULT 6
US-09-998-598-2593
; Sequence 2593, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 2593
; LENGTH: 1531

TYPE: PRT
ORGANISM: Homo sapiens
US-09-998-2593

Query Match 100.0%; Score 49; DB 9; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
|||||||
Db 828 FLYDDNORV 836

RESULT 7
US-10-171-311-222

Sequence 222, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersch, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 222
LENGTH: 1531
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-222

Query Match 100.0%; Score 49; DB 14; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
|||||||
Db 828 FLYDDNORV 836

RESULT 8
US-10-301-822-211

Sequence 211, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MEM01-0292RMM
CURRENT APPLICATION NUMBER: US/10/301,822

CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 1531
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-211

Query Match 100.0%; Score 49; DB 14; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
|||||||
Db 828 FLYDDNORV 836

RESULT 9
US-10-435-696-46
Sequence 46, Application US/10435696
Publication No. US20040018525A1
GENERAL INFORMATION:
APPLICANT: Wirtz, Ralph
APPLICANT: Munnes, Marc
APPLICANT: Kallabis, Harald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
FILE REFERENCE: Lea 36 108
CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP03003112.4
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: EP02010291.9
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46
LENGTH: 1531
TYPE: PRT
ORGANISM: Homo sapiens
US-10-435-696-46

Query Match 100.0%; Score 49; DB 15; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
|||||||
Db 828 FLYDDNORV 836

RESULT 10
US-10-723-860-2100

Sequence 2100, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05887.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 2100
LENGTH: 1531
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-2100

Query Match 100.0%; Score 49; DB 17; Length 1531;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 828 FLYDDNORV 836

RESULT 11
US-10-296-115-1161
Sequence 1161, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: NO. US20040053248A1 Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296.115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488.725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552.317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1161
LENGTH: 1621
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: msec feature
LOCATION: (1) _ (1621)
OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
US-10-296-115-1161

Query Match 100.0%; Score 49; DB 15; Length 1621;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 844 FLYDDNORV 852

RESULT 12
US-10-408-765A-3017
Sequence 3017, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Rahy, Bohn D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408.765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3017
LENGTH: 1626
TYPE: PRT

ORGANISM: Homo sapiens
US-10-408-765A-3017

Query Match 100.0%; Score 49; DB 16; Length 1626;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 849 FLYDDNORV 857

RESULT 13
US-10-369-493-5435
Sequence 5435, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369.493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360.039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5435
LENGTH: 816
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5435

Query Match 81.6%; Score 40; DB 14; Length 816;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
DB 436 FLYDDNORV 444

RESULT 14
US-10-369-493-5596
Sequence 5596, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369.493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360.039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5596
LENGTH: 1520
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5596

Query Match 81.6%; Score 40; DB 14; Length 1520;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Mon Jan 3 13:32:55 2005

QY 1 FLYDDNORV 9
|||:||||:
Db 863 FLYEENORI 871

RESULT 15
US-10-369-493-5597
; Sequence 5597, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5597
; LENGTH: 1520
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5597

Query Match 81.6%; Score 40; DB 14; Length 1520;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
|||:||||:
Db 863 FLYEENORI 871

Search completed: December 29, 2004, 16:42:49
Job time : 145 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 16:21:45 ; Search time 38 Seconds
(without alignments)
22.788 Million cell updates/sec

Title: US-10-006-177-4

Perfect score: 49

Sequence: 1 FLYDDNORV 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	227	2	A48536 DNA topoisomerase
2	49	100.0	227	2	B48536 DNA topoisomerase
3	49	100.0	1526	2	JN0598 DNA topoisomerase
4	49	100.0	1526	2	A44406 DNA topoisomerase
5	49	100.0	1528	2	J50703 DNA topoisomerase
6	49	100.0	1530	2	A40493 DNA topoisomerase
7	49	100.0	1612	2	S59699 DNA topoisomerase
8	49	100.0	1626	2	A39242 DNA topoisomerase
9	41	83.7	558	2	AB1236 glycerol 3 phosphatase
10	40	81.6	816	2	C88196 protein xk127.7 [
11	40	81.6	1520	2	T23620 hypothetical prote
12	37	75.5	80	2	T00184 hypothetical prote
13	37	75.5	82	2	G85987 hypothetical prote
14	37	75.5	112	1	L6H0AR Ig lambda chain V-
15	36	73.5	329	2	T21844 hypothetical prote
16	36	73.5	968	2	D87570 exinuclease ABC.
17	36	73.5	1711	2	T18429 hypothetical prote
18	35	71.4	558	2	AB1599 glycerol 3 phosphatase
19	35	71.4	659	2	F70175 rep helicase, sing
20	35	71.4	698	2	T35162 transketolase - St
21	34	69.4	88	2	H89858 conserved hypotet
22	34	69.4	102	1	HSTR41 histone H4, major
23	34	69.4	102	1	HSTR42 histone H4, minor
24	34	69.4	103	2	A25875 histone H4 - Tetra
25	34	69.4	151	2	A97008 transcription regu
26	34	69.4	229	2	T09824 fiber protein 3 [i
27	34	69.4	252	2	AB1748 acetyltransferase hom
28	34	69.4	252	2	AB1748 acetyltransferase hom
29	34	69.4	275	2	T09822 fiber protein 2 [i

30	34	69.4	307	2	S75461 hypothetical prote
31	34	69.4	331	2	T09820 fiber protein 1 [i
32	34	69.4	485	2	C64680 hypothetical prote
33	34	69.4	494	2	S75398 lysine-tRNA ligase
34	34	69.4	618	2	T28668 hypothetical prote
35	33	67.3	88	2	H84078 hypothetical prote
36	33	67.3	131	1	L6H0EB Ig lambda chain pr
37	33	67.3	286	2	D86163 P15K9.19 protein -
38	33	67.3	294	2	D85036 hypothetical prote
39	33	67.3	393	2	T21295 hypothetical prote
40	33	67.3	396	1	B69851 cytochrome P450 [y]
41	33	67.3	410	2	T06665 hypothetical prote
42	33	67.3	432	2	S83394 fumarylacetoacetas
43	33	67.3	476	2	T46067 hypothetical prote
44	33	67.3	573	2	H89904 aerobic glycerol-3
45	33	67.3	617	2	G81338 probable primosoma

ALIGNMENTS

RESULT 1

A48536 DNA topoisomerase II type A - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1998
C:Accession: A48536
R:Tsutsui, K.; Tsutsui, K.; Okada, S.; Watanabe, M.; Shohmori, T.; Seki, S.; Inoue, Y.
J. Biol. Chem. 268, 19076-19083, 1993
A>Title: Molecular cloning of partial cDNAs for rat DNA topoisomerase II isoforms and t
A:Reference number: A48536; MUID:93366832; PMID:8395528
A:Accession: A48536
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-227 <TSU>
A:Experimental source: Sprague-Dawley, brain
A>Note: Sequence extracted from NCBI backbone (NCBIN:136742, NCBI:136745)
C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hy
C:Keywords: ATP

Query Match 100.0%; Score 49; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
Db 91 FLYDDNORV 99

RESULT 2

B48536 DNA topoisomerase II type B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B48536
R:Tsutsui, K.; Tsutsui, K.; Okada, S.; Watanabe, M.; Shohmori, T.; Seki, S.; Inoue, Y.
J. Biol. Chem. 268, 19076-19083, 1993
A>Title: Molecular cloning of partial cDNAs for rat DNA topoisomerase II isoforms and t
A:Reference number: A48536; MUID:93366832; PMID:8395528
A:Accession: B48536
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-227 <TSU>
A:Cross-references: UNIPROT:Q63177
A:Experimental source: Sprague-Dawley, brain
A>Note: Sequence extracted from NCBI backbone (NCBIN:136743, NCBI:136746)
C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hy
C:Keywords: ATP

Query Match 100.0%; Score 49; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
|||||
Db 91 FLYDDNORV 99

RESULT 3

JN0598
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - rat
N/Alternate names: DNA topoisomerase II
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C/Accession: JN0598; S32012
R/Parc: S.H.; Yoon, J.H.; Kwon, Y.D.; Park, S.D.
Biochem. Biophys. Res. Commun. 193, 787-793, 1993
A/Title: Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II.
A/Reference number: JN0598; MUID:93290677; PMID:8350253
A/Accession: JN0598
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-1526 <PAR>
A/Cross-references: EMBL:Z19552; NID:957963; PIDN:CA479611.1; PID:957964
A/Experimental source: testis
A/Note: the authors translated the codon GTG for residue 3 as Leu
C/Comment: This enzyme is required for the segregation of circular DNA molecules after r
C/Genetics:
A/Genes: rTOP2
C/Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C/Keywords: ATP; DNA recombination; DNA repair; DNA replication; isomerase
F/689-916/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 100.0%; Score 49; DB 2; Length 1526;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
|||||
Db 826 FLYDDNORV 834

RESULT 4

A44406
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - Chinese hamster
N/Alternate names: DNA-gyrase; type II DNA topoisomerase
C/Species: Cricetus griseus (Chinese hamster)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A44406
R/Chan: V.T.; Ng, S.W.; Eder, J.P.; Schnipper, L.E.
J. Biol. Chem. 268, 2160-2165, 1993
A/Title: Molecular cloning and identification of a point mutation in the topoisomerase II
A/Reference number: A44406; MUID:93131977; PMID:8380592
A/Accession: A44406
A/Molecule type: nucleic acid
A/Residues: 1-1526 <CHA>
A/Cross-references: UNIPROT:P41515; GB:L04607; NID:9191217; PIDN:AAA37023.1; PID:9191218
A/Experimental source: ovary
A/Note: Sequence extracted from NCBI backbone (NCBIP:123211)
C/Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C/Keywords: ATP; DNA binding; DNA replication; heterodimer; isomerase

Query Match 100.0%; Score 49; DB 2; Length 1526;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
|||||
Db 827 FLYDDNORV 835

RESULT 5

J50703
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - mouse
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C/Accession: J50703; S35483
R/Adachi, N.; Miyake, M.; Ikeda, H.; Kikuchi, A.
submitted to JIPID, July 1992
A/Reference number: J50703
A/Accession: J50703
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-1528 <ADA>
A/Cross-references: UNIPROT:Q001320; DDBJ:DJ2513; NID:9220615; PIDN:BA402076.1; PID:9220616
R/Adachi, N.; Miyake, M.; Ikeda, H.; Kikuchi, A.
Nucleic Acids Res. 20, 5297-5303, 1992
A/Title: Characterization of cDNA encoding the mouse DNA topoisomerase II that can comp
A/Reference number: S35483; MUID:93065194; PMID:1331984
A/Accession: S35483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1528 <ADA2>
A/Cross-references: EMBL:DJ2513; NID:9220615; PIDN:BA402076.1; PID:9220616
C/Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hy
C/Keywords: ATP; DNA binding; isomerase; leucine zipper; nucleus
F/994-1015/Region: leucine zipper motif
F/804/Active site: Tyr #status predicted

Query Match 100.0%; Score 49; DB 2; Length 1528;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
|||||
Db 827 FLYDDNORV 835

RESULT 6

A40493
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) alpha - human
C/Species: Homo sapiens (man)
C/Date: 07-Feb-1992 #sequence_revision 03-Apr-1992 #text_change 19-Dec-1998
C/Accession: A40493; A41278
R/Tsai-Pflugfelder, M.; Liu, L.F.; Liu, A.A.; Tewey, K.M.; Whang-Peng, J.; Knutsen, T.;
Proc. Natl. Acad. Sci. U.S.A. 85, 7177-7181, 1988
A/Title: Cloning and sequencing of cDNA encoding human DNA topoisomerase II and localiz
A/Reference number: A40493; MUID:89017161; PMID:2845399
A/Accession: A40493
A/Molecule type: mRNA
A/Residues: 1-1530 <TSA>
A/Cross-references: GB:J04088
R/Bugs, B.T.; Danko, M.K.; Beck, W.T.; Suttle, D.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 7654-7658, 1991
A/Title: Expression of a mutant DNA topoisomerase II in CCRF-CEM human leukemic cells a
A/Reference number: A41278; MUID:91352047; PMID:1652758
A/Accession: A41278
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 442-521 <BUG>
A/Note: a mutant with residue 449-Arg replaced by Gln was resistant to teniposide
C/Genetics:
A/Genes: GDB:TOP2A; TOP2
A/Cross-references: GDB:118884; OMIM:126430
A/Map position: 17q21-17q22
C/Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hy
C/Keywords: ATP; DNA binding; isomerase; nucleus

Query Match 100.0%; Score 49; DB 2; Length 1530;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
|||||
Db 827 FLYDDNORV 835

RESULT 7

S59969

DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) isoform beta - Chinese hamster
 N:Alternate names: DNA topoisomerase II isoform beta; DNA-gyrase
 C:Species: *Cricetus griseus* (Chinese hamster)
 C>Date: 15-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
 A:Accession: S59969; S54154
 R:Derivative: S.; Frey, S.; Delaporte, C.; Jacquemin-Sablon, A.
 B:Location: Biophys. Acta 1264, 178-182, 1995
 A:Title: Cloning and characterization of full-length cDNAs coding for the DNA topoisomerase II
 A:Reference number: S59969; MUID:96085121; PMID:7495861
 A:Accession: S59969
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-1612 <DER>
 A:Cross-references: EMBL:X86455; NID:9790987; PIDN:CAA60173.1; PID:9790988
 A:Experimental source: lung
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
 C:Keywords: ATP; DNA binding; DNA replication; isomerase; nucleus
 F:697-927/Domains: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 100.0%; Score 49; DB 2; Length 1612;
 Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
 Db 837 FLYDDNORV 845

RESULT 8
 A39242
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) beta, splice form 2 - human
 N:Alternate names: DNA topoisomerase II isoform beta-2
 C:Species: *Homo sapiens* (man)
 C>Date: 04-Oct-1991 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 A:Accession: S26730; A39242; S10710; S33970; S30191; S41641; S30190
 R:Jenkins, J.R.; Aytton, P.; Jones, T.; Davies, S.L.; Simmons, D.L.; Harris, A.L.; Sheer,
 Nucleic Acids Res. 20, 5587-5592, 1992
 A:Title: Isolation of cDNA clones encoding the beta isozyme of human DNA topoisomerase I
 A:Reference number: S26730; MUID:93087165; PMID:1333583
 A:Accession: S26730
 A:Molecule type: mRNA
 A:Residues: 1-23,29-1626 <JEN>
 A:Cross-references: UNIPROT:Q02880; EMBL:X68060; NID:937230; PIDN:CAA48197.1; PID:937231
 R:Chung, I.D.Y.; Drake, F.H.; Tan, K.B.; Per, S.R.; Crooke, S.T.; Mirabelli, C.K.
 Proc. Natl. Acad. Sci. U.S.A. 86, 9431-9435, 1989
 A:Title: Characterization and immunological identification of cDNA clones encoding two h
 A:Reference number: A39242; MUID:90083281; PMID:2556712
 A:Accession: A39242
 A:Molecule type: mRNA
 A:Residues: 149-1043 <CHU>
 A:Cross-references: GB:M27504
 R:Austin, C.A.; Fisher, L.M.
 FEBS Lett. 266, 115-117, 1990
 A:Title: Isolation and characterization of a human cDNA clone encoding a novel DNA topoi
 A:Reference number: S10710; MUID:90306333; PMID:2163884
 A:Accession: S10710
 A:Molecule type: mRNA
 A:Residues: 1043-1276 <AUS>
 A:Cross-references: GB:X53662; GB:S56813; NID:938324; PIDN:CAA37706.1; PID:938325
 R:Austin, C.A.; Sing, J.H.; Patel, S.; Fisher, L.M.
 Biochim. Biophys. Acta 1172, 283-291, 1993
 A:Title: Novel HeLa topoisomerase II is the II-beta isoform: complete coding sequence ar
 A:Reference number: S30190; MUID:93192319; PMID:8383537
 A:Accession: S33970
 A:Molecule type: mRNA
 A:Residues: 1-23,29-1610, 'A', 1612-1626 <AU2>
 A:Cross-references: EMBL:Z15111
 R:Austin, C.A.; Sing, J.H.; Patel, S.; Fisher, L.M.
 Submitted to the EMBL Data Library, September 1992
 A:Reference number: S30191
 A:Accession: S30191
 A:Molecule type: mRNA

A:Residues: 596-1430, 'S', 1432-1610, 'A', 1612-1626 <AU1>
 A:Cross-references: EMBL:Z15115; NID:9288564; PIDN:CAA70821.1; PID:9288565
 R:Davis, S.L.; Jenkins, J.R.; Hickson, I.D.
 Nucleic Acids Res. 21, 3719-3723, 1993
 A:Title: Human cells express two differentially spliced forms of topoisomerase II-beta
 A:Reference number: S41641; MUID:93376494; PMID:8396237
 A:Accession: S41641
 A:Molecule type: DNA
 A:Residues: 24-80 <DAV>
 A:Cross-references: EMBL:X71911; NID:9396540; PIDN:CAA50726.1; PID:93960296
 A:Note: this sequence represents a long minor splice form, designated beta-2
 C:Genetics:
 A:Gene: GDB:TOP2B
 A:Cross-references: GDB:131575; OMIM:126431
 A:Map position: 3p24-3p24
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hy
 C:Keywords: alternative splicing; ATP; dimer; isomerase; nucleus
 F:1-1626/Product: DNA topoisomerase II beta-2 status predicted <MNR>
 F:1-23,29-1626/Product: DNA topoisomerase II beta-1 status predicted <MAJR>
 F:709-939/Domains: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T

Query Match 100.0%; Score 49; DB 2; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
 Db 849 FLYDDNORV 857

RESULT 9
 AE1236
 glycerol 3-phosphate dehydrogenase homolog glpD [imported] - *Listeria monocytogenes* (st
 C:Species: *Listeria monocytogenes*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 A:Accession: AE1236
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Bagnero, F.; Berche, P.; Bloecke
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Ficht, H
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schluter, T.; Simoes, N.; Tixeront, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AE1236
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-558 <GLA>
 A:Cross-references: UNIPROT:Q8Y714; GB:NC_003210; PIDN:CA093971.1; PID:916410709; GSPDB
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: glpD
 C:Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)

Query Match 83.7%; Score 41; DB 2; Length 558;
 Best Local Similarity 77.8%; Pred. No. 4.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDDNORV 9
 Db 199 FLYDDNORV 207

RESULT 10
 C88196
 protein ZK1127.7 [imported] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 A:Accession: C88196
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolo
 A:Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: C88196
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-816 <STO>
A/Cross-references: UNIPROT:Q27537; GB:chr II; PIDN:AB93429.1; PID:g13j30372; GSPDB:GN000
A/Note: strong similarity to DNA topoisomerase II
C/Genetics:
A/Map position: 2

Query Match 81.6%; Score 40; DB 2; Length 816;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 436 FLYENORI 444

RESULT 11

hypothetical protein K12D12.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23620; T26109
R/Colles, L.

Submitted to the EMBL Data Library, April 1995
A/Reference number: Z19772

A/Accession: T23620
A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-1520 <WIL>

A/Cross-references: UNIPROT:Q23670; EMBL:Z49069; PIDN:CAA8867.1; GSPDB:GN00020; CESP:K1

A/Experimental source: clone K12D12

R/Swindburne, J.

Submitted to the EMBL Data Library, March 1996

A/Reference number: Z20470

A/Accession: T28109
A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-1520 <W12>

A/Cross-references: EMBL:Z70213; PIDN:CAA94177.1; GSPDB:GN00020; CESP:K12D12.1

A/Experimental source: clone ZK930

C/Genetics:

A/Map position: 2

A/Accession: T28109

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-1520 <W12>

A/Cross-references: EMBL:Z70213; PIDN:CAA94177.1; GSPDB:GN00020; CESP:K12D12.1

A/Experimental source: clone ZK930

C/Genetics:

A/Residues: 1-80 <KAN>
A/Cross-references: UNIPROT:O80089; EMBL:AB009866; NID:d1204727; PIDN:BAA31924.1; PID:d1
Query Match 75.5%; Score 37; DB 2; Length 80;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 19 YLYQDNERV 27

hypothetical protein SA1786 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G89987
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu-
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; NID:21311952; PMID:11418146

A/Accession: G89987

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-82 <KUR>

A/Cross-references: UNIPROT:Q998S5; GB:BA000018; PID:g13j701771; PIDN:BAA3064.1; GSPDB:K

A/Experimental source: strain N315

C/Genetics:

A/Map position: 2

A/Accession: G89987

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-82 <KUR>

A/Cross-references: UNIPROT:Q998S5; GB:BA000018; PID:g13j701771; PIDN:BAA3064.1; GSPDB:K

A/Experimental source: strain N315

C/Genetics:

A/Map position: 2

A/Accession: G89987

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-82 <KUR>

A/Cross-references: UNIPROT:Q998S5; GB:BA000018; PID:g13j701771; PIDN:BAA3064.1; GSPDB:K

A/Experimental source: strain N315

C/Genetics:

A/Map position: 2

A/Residues: 1-80 <KAN>
A/Cross-references: UNIPROT:O80089; EMBL:AB009866; NID:d1204727; PIDN:BAA31924.1; PID:d1
Query Match 75.5%; Score 37; DB 2; Length 80;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDDNORV 9
Db 19 YLYQDNERV 27

hypothetical protein SA1786 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G89987
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu-
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; NID:21311952; PMID:11418146

A/Accession: G89987

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-82 <KUR>

A/Cross-references: UNIPROT:Q998S5; GB:BA000018; PID:g13j701771; PIDN:BAA3064.1; GSPDB:K

A/Experimental source: strain N315

C/Genetics:

A/Map position: 2

A/Accession: G89987

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-82 <KUR>

A/Cross-references: UNIPROT:Q998S5; GB:BA000018; PID:g13j701771; PIDN:BAA3064.1; GSPDB:K

A/Experimental source: strain N315

C/Genetics:

A/Map position: 2

A/Accession: G89987

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-82 <KUR>

A/Cross-references: UNIPROT:Q998S5; GB:BA000018; PID:g13j701771; PIDN:BAA3064.1; GSPDB:K

A/Experimental source: strain N315

C/Genetics:

A/Map position: 2

Oy 2 LYDDNQR 8
:|||||
Db 49 IYDDNQR 55

RESULT 15

T21844
hypothetical protein F36D1.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21844
R:Harris, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19477
A:Accession: T21844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-329 <WIL>
A:Cross-references: UNIPROT:Q9XV37; EMBL:Z81530; PIDN:CAB04310.1; GSPDB:GN00019; CESP:F3
A:Experimental source: clone F36D1
C:GeneticB:
A:Gene: CESP:F36D1.8
A:Map position: 1
A:introns: 60/1; 75/3; 123/2; 167/2; 214/2; 267/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F49D11.3

Query Match 73.5%; Score 36; DB 2; Length 329;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FLYDDNQ 7
:|||||
Db 101 FLYDDNQ 107

Search completed: December 29, 2004, 16:31:13
Job time : 39 secs

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